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Minimum DB
Maximum DB
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: pir1:*
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   Query
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Copyright (c) 1993 - 2000
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Compugen Ltd
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Ig kappa ch

Ig kappa ch
 19
19
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g kappa chain - m
onoclonal antibod
g kappa chain V r
g kappa chain pre
g kappa chain - m
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g kappa chain - m
g kappa chain (Ma)
g kappa chain V r
g kappa chain v r
g kappa chain nore
g kappa chain v r
g kappa chain v r
g kappa chain NIG
g kappa chain NIG
g kappa chain NIG
g kappa chain NIG
g kappa chain V-C
g kappa chain Pre
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
463.5	464.5	464.5	466	466	468.5	469	469.5	471.5	475.5	479	484	484.5	484.5	493	497.5
41.3	41.4	41.4	41.6	41.6	41.8	41.8	41.9	42.1	42.4	42.7	43.2	43.2	43.2	44.0	44.4
216	233	108	236	213	113	106	130	228	109	233	106	130	109	217	140
ν	N	N	N	N	N	ᆫ	N	N	N	2	<u> </u>	N	N	N	N
S29258	S25744	PL0278	S25746	S21066	S03410	K1RTB	S04573	S29575	PT0404	S29577	Klrta	A32513	PT0405	JE0246	PL0013
Ig lambda	Ig lambda	Ig kappa	Ig lambda	Ig lambda	Ig kappa	Ig kappa	Ig kappa	Ig light	Ig light	Ig light	Ig kappa	. Ig kappa	Ig light	. Ig lambda	Ig kappa
		chain V r	a chain -	a chain V	chain pre	chain C r	chain pre	chain - r	chain V r	chain - r	chain C r	chain pre	chain V r	a chain NI	chain pre

ALIGNMENTS

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monoclonal antibody 13-1 light chain - mouse C;Species: Mus musculus (house mouse) C;Date: 04-Feb-1998 *sequence_revision 13-Mar-1998 *text_change 21-Jan-2000 C;Accession: JC5810 R;Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M. Biochem. Biophys. Res. Commun. 240, 566-572, 1997 A;Title: Structural characterization of mouse monoclonal antibody 13-1 again A;Reference number: JC5810; MUID:98063277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-235 <FIS>
A; Cross-references: EMBL:X67211; NID:g54828; PIDN:CAA47650.1; PID:g54829
C; Superfamily: immunoglobulin V region; immunoglobulin homology
F; 38-111/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            $25058

$19 kappa chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000
C;Accession: $25058
R;Fischer, R: Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzale submitted to the EMBL Data Library, July 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
A; Molecule type: protein
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Best Local Similarity
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he EMBL Data Library, July 1992
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                                                                    566-572, 1997
n_of_mouse monoclonal antibody 13-1 against a
                                                                                               Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada,
66-572, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; DB 2;
.5e-55;
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against

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$68241

Ig kappa chain V region (Mabl3-1) - mouse (fragment)
N;Alternate names: immunoglobulin light chain
C;Species: Mus musculus (house mouse)
C;Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-218 <AKA>
C;Comment: This catalytic antibody has peroxidase oxidase. It is directed C;Superfamily: immunoglobulin V region; immunoglobulin homology F;16-94/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-220 <SCH>
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Best Local S
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                                                                                                                                     STLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC
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                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                         79.0%;
78.4%;
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Pred. No. 6.1e-49;
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SGSGSGQDYSLTISSLEYEDVGVYYCLRYDEFPFTFGSGTKLEIKRADAAPTVSIFPPSS

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C;Species: Mus musculus (house mouse)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S14237
R;Vandanme, A.M.; Bulens, F.; Bernar, H.; Nelles, L.; Lijnen, R.H.; Collen, Bur. J. Biochem. 192, 767-775, 1990
A;Title: Construction and characterization of a recombinant murine monoclona A;Reference number: S14236; MUID:91006173
A;Accession: S14237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-234 < VAN>
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R;Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, FEBS Lett. 375, 273-276, 1995
A;Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyr A;Reference number: S68211; MUID:96085223
A;Reference number: S68211; MUID:96085223
A;Accession: S68214
A;Status: nucleic acid sequence not shown
A;Residues: 'NI',3-212 <TAW>
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R;Takagi, M.; Köhda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.;
submitted to the EMBL Data Library, March 1994
A;Description: Specific peroxidase activity by formation of an a
A;Reference number: S68241
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A; Residues: 1-218 <TAK>
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Best Local Similarity
Matches 172; Conser
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Best Local Similarity
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                                                                                                                             LTQSPAIMSASPGEKVTMTCRASSSVSSSYLHWYRQKSGASPKLWIYSTSNLASGVPARF 63
SGSGSGTSYSLTISSVEAEDAATYYCQQYSGYR-TFGGGTKLEIKRADAAPTVSIFPPSS 122
                                                                                         MTQSPSSMYASLGERVTVTCKASQDI-NSYLSWIQQKPGKSPKTLIYRGNRLVAGVPSRF 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC
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79.7%;
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78.9%;
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Pred. No. 2.3e
L5; Mismatches
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Pred. No. 9.
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.2e-49;
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1g kappa chain - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Date: 06-Jan-1995 #sequence_revision
C; Accession: S38865
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A; Residues: 1-225 <DUC>
A; Residues: 1-225 <DUC>
A; Cross-references: EMBL: X70424; NID: g406254; PIDN: CAA49869.1; PID: g406255
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
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                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-219 <KIP>
                                                                                                                                                                                    submitted to the EMBL Data A; Description: Combination A; Reference number: S38864 A; Accession: S38865
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Ig kappa chain –
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Best Loc
Matches
                                                                                             Cross-references: EMBL:227396; NID:g416538; PIDN:CAA81787.1; PID:g416539; Superfamily: immunoglobulin V region; immunoglobulin homology; Keywords: heterotetramer; immunoglobulin
                             Query Match
Best Local Similarity
Matches 169; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g kappa chain - mouse (fragment)
;Species: Mus musculus (house mouse)
;Date: 06-Jan-1995 #sequence_revision
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                               Conservative
                                         77.6%;
77.2%;
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79.3%;
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                             16;
                                         Score 869.5; DB 2;
Pred. No. 6.5e-48;
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                                         A; Reference number: PC4202; A; Accession: PC4203
                                                      R:Kwak, J.W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Gene 173, 257-259, 1994 and characterization of cDNAs coding for A; Title: Cloning and characterization of cDNAs coding for A; Reference number: PC4202; MUID:97082978
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              A; Molecule type: mRNA
A; Residues: 1-219 < KWA>
                                                                                                                                                                                                                               В
A;Cross-references: GB:U29147; NID:g1594225; PIDN:AAC52821.1; PID:g1594226
                                                                                                                C; Accession: PC4203
                                                                                                                                                                        PC4203
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Ig kappa chain (monoclonal antibody MabA34) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 11-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X13187; NID:g51784; PIDN:CAA31579.1; A;NOte: this sequence was determined from the differentiated g C;Superfantly: immunoglobulin V region; immunoglobulin homolog C;Keywords: heterotetramer; immunoglobulin immunoglobulin F;1-20/Domain: signal sequence #status predicted <SIG>F;1-20/Domain: Ig kappa chain #status predicted <MAT>F;36-110/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig kappa chain precursor - mouse

C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 21-Jan-2000
C;Accession: S01320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-234 <DE1>
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A;Accession: S01320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, Eur. J. Biochem. 176, 287-295, 1988
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 214
                                                                                                                                                                                                            KDEYERHNSYTCEATHKTSTSPIVKSFNRNEC
                                                                                                                                                                                                                                      KDEYERHNSYTCEATHKTSTSPIVKSFNRNEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGSGSGTSYSLTISSVEAEDAATYYCQQY-SGYRTFGGGTKLEIKRADAAPTVSIFPPSS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MTQSPASLSVSVGESVTITCRASENIYSN-LAWYQQKQGKSPQLLVYVATKLVDGVPSRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                   SGSGSGTQYSLKINSLQSEDFGSYYCQHFWDTPFTFGSGTKLEMKRADAAPTVSIFPPSS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77.5%; Score 869; DB 2; 78.3%; Pred. No. 7.4e-48; tive 19; Mismatches 25
                                                                                                                                                                                                                                                                 214
                                                                                                                                                                                                            234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 234;
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S.H.; Park,

heavy

and light chains Y.B.; Han,

of

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Ig kappa chain V region (clone 23.2) - C;Species: Mus musculus (house mouse) C;Date: 19-Oct-1995 #sequence_revision
                                              RESULT
A56169
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A; Residues: 1-219 <VAN>
A; Residues: 1-219 <VAN>
A; Cross-references: EMBL:L35138; NID:g522336; PIDN:AAA67525.1;
A; Cross-references: EMBL:L35138; NID:g522336; PIDN:AAA67525.1;
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 16-95/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig kappa chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change
C;Accession: S52028
R;van Engelen, F.; Schouten, A.; Molthoff, J.W.; Roosien, J.; Di
submitted to the EMBL Data Library, August 1994
A;Description: Coordinate expression of antibody subunit genes y
A;Accession: S52028
A;Accession: S52028
A;Status: preliminary
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Best Local Similarity
Matches 168; Conser
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Best Local Similarity
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                                                                                                                                                                                                                                          VPARFSGSGSGTSYSLTISSVEAEDAATYYCQQYSGY-RTFGGGTKLEIKRADAAPTVSI 117
                                                                                                                                                                                                                                                                                                    VLTQSPAIMSASPGEKVTMTCRASSSV----SSSYLHWYRQKSGASPKLWIYSTSNLASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FPPSSEQLTSGGASVVCFLNNFYPRDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSS 177
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                                                                                                                                                                                FPPSSEQLTSGGASVVCFLNNFYPRDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSS
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                                                                                                                                                                  FPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSS
                                                                                                                                                                                                                           VPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPPTFGGGTNLEIKRADAAPTVSI 122
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77.48;
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77.48;
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                                                                                                                                                                                                                                                                                                                                           Score 861.5;
Pred. No. 2e-4
14; Mismatches
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Pred.
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                                 mouse
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No. 2e-47;
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                                (fragment)
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Ly mappa chain (Mab03-1) - mouse (fragi
C.Species: Mus musculus (house mouse)
C.Date: 29-Jul-1997 #sequence_revision
C.Accession: S68212
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R; Monfardini, C.; Kieber-Emmons, T.; VonFeldt, J.M.; O'Malley, E
J. Biol. Chem. 270, 6628-6638, 1995
A; Title: Recombinant antibodies in bioactive peptide design.
A; Reference number: A56169; MUID:95204454
A; Accession: A56169
A; Status: preliminary; not compared with conceptual translation
A; Molecule type: mRNA
A; Residues: 1-210 <MON>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                      R:Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; FEBS Lett. 375, 273-276, 1995

A:Title: Thermostable peroxidase activity with a recombinant antibody L chair A; Reference number: S68211; MUID:96085223

A; Accession: S68212

A; Status: preliminary; nucleic acid sequence not shown A; Molecule type: mRNA
A; Residues: 1-214 < TAK>
A; Cross-references: EMBL:D29668
C; Superfamily: immunoglobulin V region; immunoglobulin homology
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S68212
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Best Local
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Best Local :
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                  177
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les 166; Conser
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                                                    LTLTKDEYERHNSYTCEATHKTSTSPIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PARFSGSGSGTSYSLTISSVEAEDAATYYCQQYSGYR-TFGGGTKLEIKRADAAPTVSIF 118
| |||||||| ::| | || |||||||||
| PPRFSGSGSGTDFTLNIHPVEEEDAATYYCQHSRELPWTFGGGTRLEIKRADAAPTVSIF 122
STLTLTKDEYERHNSYTCEATHKTSTSPIVKS
                                                                                                                                    GVPARFSGSGSGTSYSLTISSVEAEDAATYYCQQ-YSGYRTFGGGTKLEIKRADAAPTVS
                                                                                                                                                                                                                                                    VLTQSPAIMSASPGEKVTMTCRASSSVSSS-----YLHWYRQKSGASPKLWIYSTSNLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSST
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78.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76.4%; Score 857; DB 2; 80.3%; Pred. No. 3.8e-47;
                                                                                                                                                                                                                                                                                             18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (fragment)
                                                                                                                                                                                                                                                                                                               Score 852; DB 2; Pred. No. 7.9e-47;
                                                                                                                                                                                                                                                                                             Mismatches
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                  208
                                                                                                                                                                                                                                                                                                                               Length 214;
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F;7-225/Product: Ig kappa chain #status predicted <ILC>
F;7-106/Domain: V region #status predicted <VAR>
F;107-119/Domain: J region #status predicted <CIR>
F;120-225/Domain: C region #status predicted <COR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: strain BALB/c, cell line RP93 hybridoma cell A; Note: the authors translated the codon CGG for residue 106 as Pro, A; Note: the nucleotide sequence shown is inconsistent with authors' tect except for four positions shown above c; Comment: The protein is an anti-phosphorylcholine antibody. C; Superfamily: immunoglobulin vregion; immunoglobulin homology C; Keywords: immunoglobulin
  В
                                     δÃ
                                                                                                                                                                                     C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;16-95/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                           R; Vaesen, M.; Frosch, M.; Weisgerber, C.; Eckart, K
Biol. Chem. Hoppe-Seyler 372, 451-453, 1991
A; Title: Primary structure of the murine monoclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
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                                                                                                                                                                                                                                                        A; Molecule type: protein A; Residues: 1-219 <BIT>
                                                                                                                                                                                                                                                                                                                      A; Reference number: S16112; MUID: 92000313
A; Accession: S16112
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A; Residues: 1-225 <CHI>
                                                                                 Query Match
Best Local S
Matches 165
                                                                                                                                                                                                                                                                                                                                                                                                                              g kappa chain V region (G2a) - mouse ; Species: Mus musculus (house mouse) ; Date: 21-Nov-1993 #sequence_revision ; Accession: S16112
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Best Local Similarity
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                                                                                    Local Sin
hes 165;
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                      VLTQSPAIMSASPGEKVTMTCRASSSV----SSSYLHWYRQKSGASPKLWIYSTSNLASG 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FPPSSEQLTSGGASVVCFLNNFYPRDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSS 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VPDRFSGSGSGTDFSLEISRVEAEDLGVYYCFQSSHVRWTFGGGTKLEIKRADAAPTVSI
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VMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLYWYLQKPGQSPKPLIYRVSNRFSG 62
                                                                                 Similarity 75.7
65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76.0%;
76.5%;
                                                                                                   75.5%; Score 846.5; DB 2
75.7%; Pred. No. 1.8e-46;
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Pred. No. 8.9e-47;
                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                10-Nov-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                        Eckart, K.; Kratzin, H.; Bitter-Suermann, D.;
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                                                                                                                         DB 2;
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                                                                                                                                                                                                                                                                                                                                                              IgG2a antibody
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Search completed: Job time: 164 sec

June 18,

2001,

15:32:46

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A;Molecule type: mRNA
A;Residues: 1-217 <5CH>
A;Residues: 1-217 <5CH>
A;Cross-references: EMBL:X75536; NID:g414143; PIDN:CAA53226.1; PID:g414144
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
E;14-93/Domain: immunoglobulin homology <IMM>
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C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S42772
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S42772
Ig kappa chain -
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                                                                                                                                                                                                                                                                                             Matches
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Best Local
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 180
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                                                                                                                                                                                                                                                       3 VLTQSPAIMSASPGEKVTMTCRASSSV----SSSYLHWYRQKSGASPKLWIYSTSNLASG 58
                                                                    IFPPSSEQLTSGGASVVCFLNNFYPRDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMS 176
               STLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 214
                                                                                                                                                                   VPARFSGSGSGTSYSLTISSVEAEDAATTYCQQYSGY--RTFGGGTKLEIKRADAAPTVS 116
                                                                                                                                                                                                                     VMTQSPLSLPVSLGDQASISCRSSQSLVHTNGNTYLHWYLQKPGQSPKVLIYKVSTRFSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IFPPSSEQLTSGGASVVCFLNNFYPRDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMS 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VPDRFSGSGSGTDFTLKISRVEAEDLGVYFCFQGTHVPY-TFGGGTRLEIKRADAAPTVS
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STLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRGEC
                                                                                                                                            VPDRFSGSGSGTDFTFKISRVEAEDLGVYFCSQ-STYVPFTFGSGTKLEIKRADAAPTVS 119
                                                                                                                                                                                                                                                                                               165;
                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                           75.48;
75.78;
                                                                                                                                                                                                                                                                                             16; Mismatches
                                                                                                                                                                                                                                                                                                           Score 845.5; DB
Pred. No. 2e-46;
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